Synopsis of

CELLULAR AUTOMATA BASED COMPUTATIONAL MODELS FOR SIR EPIDEMIC SPREAD

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1.0 Introduction

Modeling of epidemics have been done using differential equations (Edelstein-Keshlet, 1988; Murray, 1993). These models did not include local characteristics of spreading process, variable susceptibility of individuals and thus unable to handle variable boundary conditions (Agiza, 1998). Although method of employing partial differential equations is available (Sleeman B.D, 2003) and social networking theory based complex system of differential equations (Meyers, 2005), these systems require large computing power and prohibitive spatial and time step constraints consideration which make them unrealistic for use in a realistic case in handling vaccination, quarantine and effect of the boundary conditions.

The model for simulating the epidemic spread (White, 2009) uses a two dimensional CA having homogeneous population and simulates the SIS model of spreading disease. The model does not have any provision for variable population or rules and did not consider the infectives for various time steps. Another model based on CA is proposed by (Sirakoulis, 2000) which handles the epidemic propagation along with population movement. The effect of vaccination in the epidemic spread is also discussed in the work but it does not deal with the extended neighborhood concept and patch population concept.

Cellular Automata based epidemic spread modeling provides the advantage of incorporating time delay and spatial factors into epidemic modeling easily when compared to the differential equation models. Epidemic spread modeling help us in understanding the dynamics of the disease spread during an epidemic and guides us during the development of vaccination, quarantine and evacuation strategies by providing the predicted results in terms of time and location of spread.

In view of the above, the aim of this research work is to develop efficient computational models through Cellular automata for modeling the epidemic spread of Susceptible-Infective-Recovered (SIR) model and apply them to various scenarios of epidemics with the factors as given above.

1.1 Cellular Automata

Non deterministic finite automata (NFA) and deterministic finite automata machines forms the basic set of computational models which has least amount of memory. An addition of stack memory to the basic model leads to a pushdown automata model popularly known as

PDA. The concepts can be used in cells of a cellular automata to form the models of epidemic spread.

A Cellular automata is a network of cells which operates in discrete time steps and is composed of the following parts

Cell C_x: Cell is the basic unit of a cellular automata. A cell could be defined as a unique space element in a one dimensional (1D) array depending upon the type of usage of the cellular of automaton. Interactions of various cells locally would evolve in to global behavior of cellular automata (Ilachinski, 2002).

States Q: The cell defined above could be in one of the finite number of states during the computation.

Transition Function $\delta: Q \rightarrow Q$ The state of the current cell in the next time step is determined by the state of the current cell along with the state of all neighborhood cells during the current time step. The state transition function for a one dimensional CA is given by the following equation(1.2).

$$C_x^{t+1} = fn(C_x^t, C_{x-1}^t, C_{x+1}^t) \qquad (1.1)$$

Neighborhood: The set of cells which are located to the left and right of the cell C_x

2.0 Motivation

In all these works discussed above and many others who have done the epidemic spread modeling using CA, the epidemic spread in patchy environment (where population live in patches) is not considered. The effect of running the rules selectively across the cells in patches were also not probed. Population heterogeneity in terms of handling infectives at various time steps and its effect in the processes of epidemic spread were not handled. These areas which are very important in implementing in CA becomes the scope of the work in this thesis. Along with these the idea of dealing the population as a two dimensional language in CA is also explored in terms of designing a two dimensional(2D) stochastic context free grammar through which we find which are the most probable productions that lead to major disease spread.

3.0 Objectives

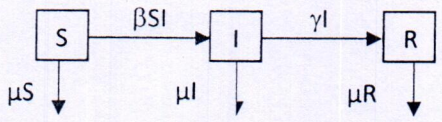
To develop and apply cellular automata (CA) models of the following types:

- 1D CA and 1D pushdown CA based epidemic spread models, to analyze the variations of spread.
- 2D CA based epidemic spread models to analyze the variations of spread for the population living in patches and explore computing time savings.
- 2D pushdown CA models for handling the latent infectives (infectives with time delay) during epidemic spread.
- 2D CA and 2D pushdown CA models for epidemic spreading based on vector borne infection.
- 3D CA model for epidemic spread as applicable in densely populated metro cities at multi-storeyed and office complexes.
- To envisage the concept of population as language and its derivation through stochastic context free epidemic spread grammar.

4.0 Description of the research work.

SIR Epidemic Model

The model named as SIR (Susceptible-Infected-Recovered) model for epidemics (Hethcote, 2000) is considered here to model a basic computational machine in terms of NFA. Susceptible are the group of population who in all probability has a chance to get the infection of a disease. Infected are the group of population who are infected with the disease. Recovered are those group of population who have recovered from the infectious disease. The following block diagram illustrates the SIR model of epidemics.

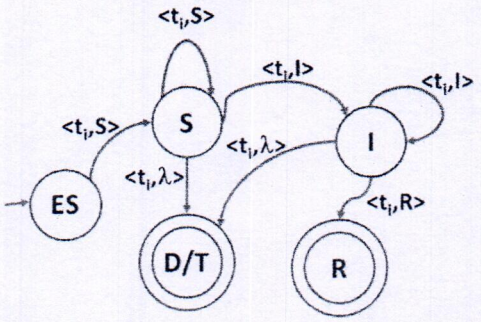


Figure[4.1] Compartmental SIR Model with constant birth and death rates

In figure[4.1] S is the number of susceptibles, I is the number of infected, R is the number of recovered, β is the infection rate, γ is the recovery rate, and μ is the birth and death assumed

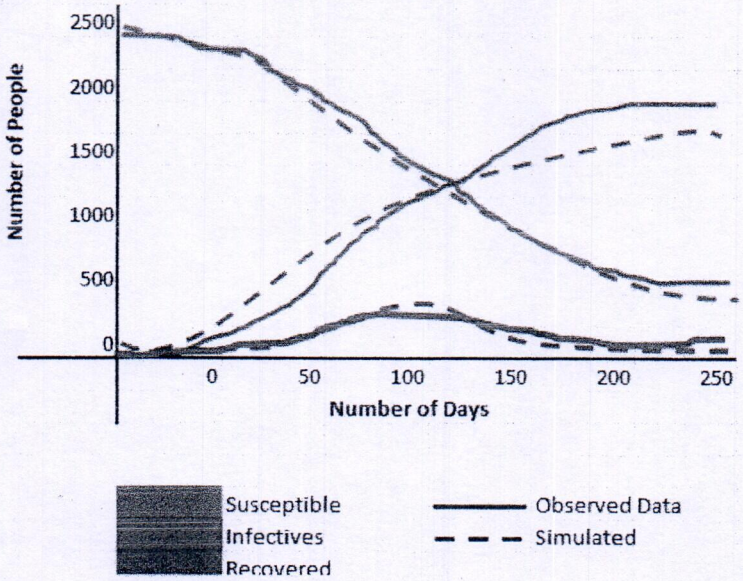
to be same during the period of the study of epidemic. If we neglect the change in overall population due to birth and death, this model reduces to that of (Kermack, 1927).

4.1 Basic Cell states using Finite Automata



Figure[4.2]: The states of the cell during an SIR epidemic

This model is run with 2500 susceptible population input and the obtained results are compared with the real time data of H1N1 2009 CDC data of Winnebago county.



Figure[4.3]: Comparison of observed and simulated data of the H1N1 Surveillance data for CDC, USA-2009 (CDC, 2009) ; (Health, 2009)

4.2 One Dimensional Cellular Automata Model

One dimensional CA model is the simplest model in which the rules operate in one dimension. The neighborhood of a particular cell consists of the cell itself and the cell

towards left side and the cell towards the right side. The following figure depicts a one dimensional cellular automata

	..	x-2	x-1	x	x+1	x+2	..	..	

Figure[4.4]: A one dimensional cellular automata

The state transition function for a one dimensional CA is given by equation(1.2)

δ(<current state of the left side cell>,<current state of the cell>,<current state of the right side cell>)➔(<state of the left cell after transition>,<state of the cell after transition>,<state of the right cell after transition>) (1.2)

The boundary cells both on the left and right will have only one neighbor, former one having on the right and the later one having on the left. The transition rules are as follows

S	S	S	➔	S	S	S
I	S	I	➔	I	I	I
S	I	S	➔	S	R	S

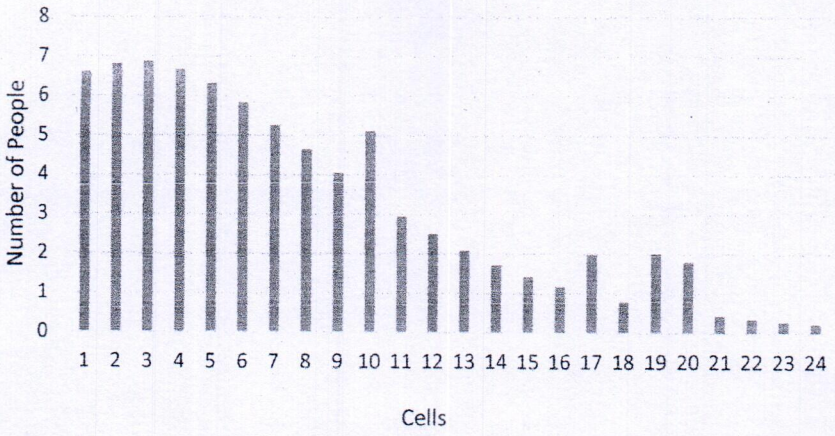
a)Rules for Non-Border Cells

S	I	➔	I	S
I	S	➔	R	S
S	S	➔	S	S

b) Rules for Border Cells

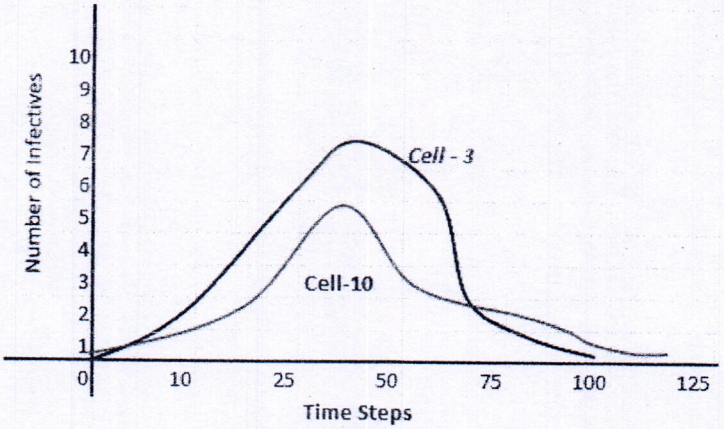
Figure[4.5]: One Dimensional Cellular Automata Rules

The transition rules are applied across a one dimensional cellular automata of size 250 cells each and each containing population size of 100. If the neighborhood radius is 1, then only right and left cell is taken in to account. As the radius increases then the probability of getting a contact with the neighborhood also decreases.



Figure[4.6(a)]: Variation of Infectives across cells in a 1D CA at time step 50.

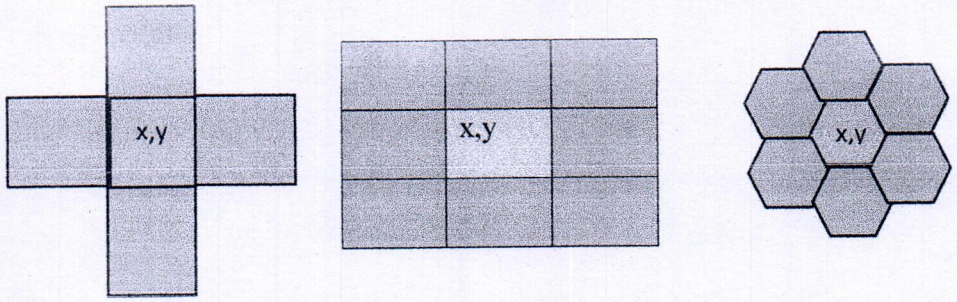
The variations of infectives at cell 3 and 10 with time is shown in figure[4.6(b)]



Figure[4.6(b)]: Variations of Infectives at cell 3 and cell 10

4.3 Two Dimensional Cellular Automata Model:

Neighborhood configurations vary in case of 2D CA models. The set of cells which are located around a cell $C_{x,y}$ are termed as neighborhood of cell $C_{x,y}$. There are different types of neighborhood configurations for a two dimensional CA, they are: von Neumann, Moore, and Hexagonal etc. which is represented in figure (4.6 (a))



a) von Neumann b) Moore c) Hexagonal

Fig [4.7(a)] Various Neighborhood configurations for the cell x,y in a 2D CA

Hexagonal and triangular grids may be considered as special cases of the nine-neighbor Moore neighborhood. Totalistic, Outer-totalistic, and additive rules are defined exactly as in the one-dimensional case, while legal rules may now be generalized to include rotation, reflection, and complexity symmetric rules.

The neighborhood structure in a 2D CA can be of either Von-Neumann or Moore neighborhood. Von-Neumann considers all the surrounding cells except the diagonal ones but Moore neighborhood considers all of them which makes the right choice for most of the epidemic situations. Following figure depicts the Moore neighborhood.

	$C_{x-1,y+1}$	$C_{x,y+1}$	$C_{x+1,y+1}$	
	$C_{x-1,y}$	$C_{x,y}$	$C_{x+1,y}$	
	$C_{x-1,y-1}$	$C_{x,y-1}$	$C_{x+1,y-1}$	

Figure[4.7(b)]: Neighborhood of a cell

The dark shaded cell is one which is the current cell. The current cell state would be updated based on the current states of the lightly shaded neighboring cells. Each cell will be having the following CSW(Cell Status Word).

Cell_id	CPV	IValue	RValue	MValue

Table 4.1: Structure of the Cell Status Word

The CSW has five parameters namely (1) Cell_id which is the current cell denoted by C(x,y), (2) Critical Population Value(CPV) which is the fraction of infected population over total

population in the cell, (3) IValue which takes Boolean value 0/1; 0 means the cell is free of infectives, 1 means some percentage of cell is infected so we consider that the cell is infected, (4) RValue will also take either 0 or 1 depending upon whether the population inside the cell is recovered from the disease or not, (5) MValue is the movement flag for a particular cell used to control the movement of the population from one cell to another. If the value is 0 it means no movement possible from the cell.

4.3.1 Homogeneous population:

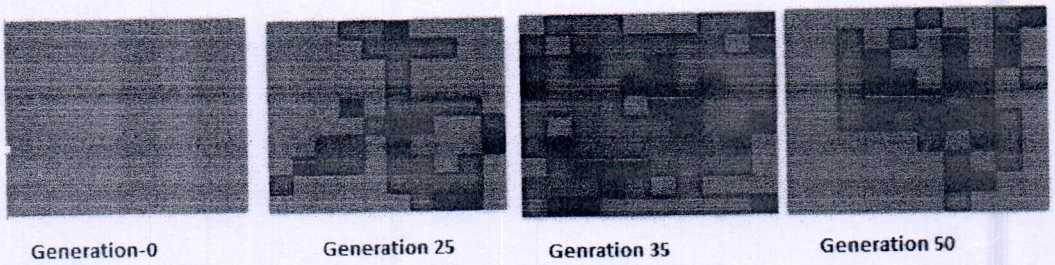


Figure 4.8: Behavior of epidemic spread across various generations in homogeneous model.

From the above figure 4.8 we observe that from the generation 0 where all cells are susceptible and then slowly the infection starts to spread and then gradually subsides in the generation 50. Here is the point to emphasize that the rules are running in all the cells and the population is assumed to be in all cells which is not true in most of the cases. The computation time taken to complete the simulation would considerably decrease when we run the rules wherever required.

4.3.2 Patch Population

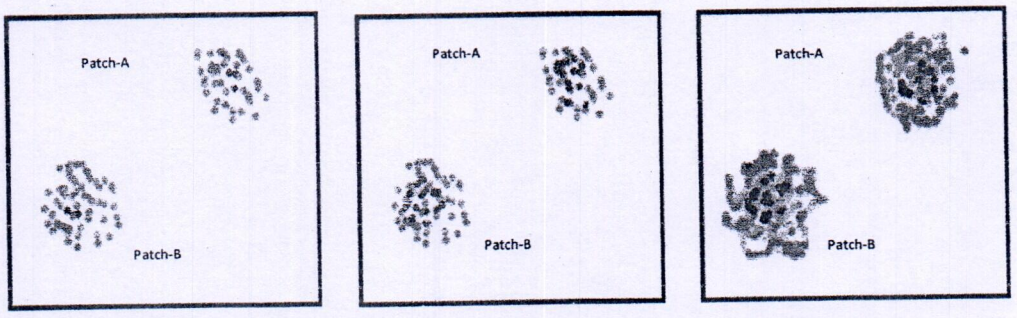
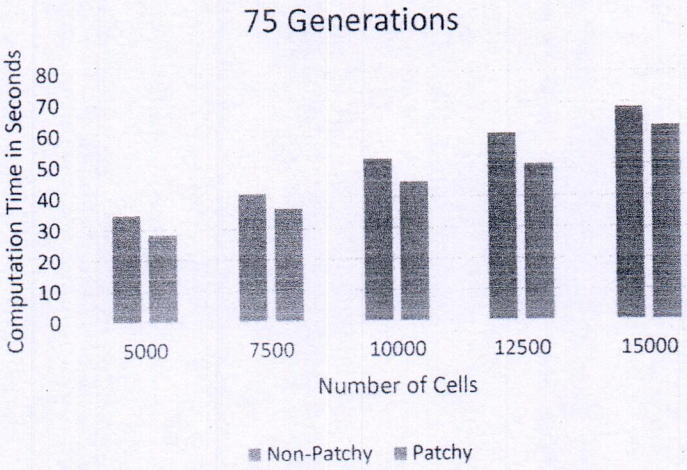


Figure [4.9]: Epidemic spread in patchy environment

The above snapshots clearly shows the spread behavior of the diseases in their respective patches.

The computation time that has been calculated across various population counts and the comparison with patchy and non-patchy environments shows us a significant decline in computation time for patchy environment. The following figure depicts that.



Figure[4.10]: Patchy Vs Non Patchy population

4.4 Two Dimensional Pushdown CA for Infectives with Time Delay

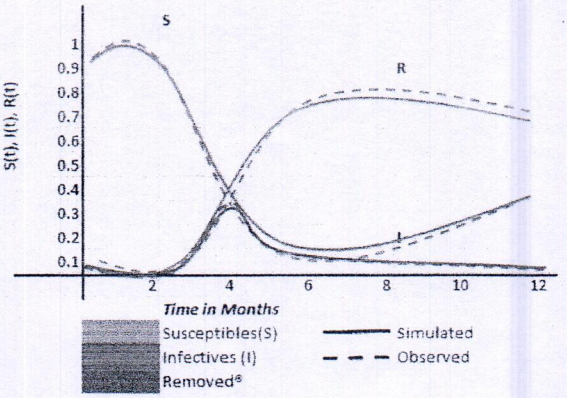
. If we consider the infected population at current time as t, then the population which were infected at the previous time steps are considered as t-1, t-2, etc. This work largely focusses on how the latent infected population, i.e the ones which are infected at t-1, t-2 has an effect in infecting the current set of susceptible population in a cell. This relates to a question-how could we segregate or handle the infected populations at t-1 or t-2? The solution is to append a stack to each cell of the cellular automaton and call the modified CA as pushdown cellular automaton or PCA (Kutrib, 1999). The idea is to hold the infective population at different time steps at different levels of stack and use them for computation for the next time step accordingly.

Cell_id		IValue	RValue	MValue

Table [4.2] Structure of the CSW at time t=2

The model is validated by the real time data of H1N1 epidemic in Abu Dhabi. The effects of quarantine and vaccination is also explored and also the variations of number of infectives over the geographical region and nature of stack content is also discussed in this work.

Figure[4.11] Mapping of cellular grid with map of Abu Dhabi[14,15]



Figure[4.12] SIR curve for the simulated and observed data

4.5 Two Dimensional CA Model for Vector Borne Infection Spread

Leptospirosis is a kind of disease where the susceptible human population is infected by infected animal population and it is not transmitted by any individual of infected human population (Shukla et al., 2014;Yang, 2007). This kind of disease spread modeling requires strategic change in the rule set of the traditional cellular automata. An idea of voting based rule on the neighborhood environment is studied for modeling the leptospirosis and compared with real data of this kind of infection in Thailand during the year 2000 and 2001.

Voting rules are the ones which update the center cell values according to the popularity of the values found in their local neighborhood (Ilachinski, 2002). Each cell in the

4.7 Stochastic Context Free Epidemic Grammar

The nature of the language the cellular automata deals with is explored and the possibility of expressing the population in terms of two-dimensional context free language is derived using the 2D stochastic context free grammar. The epidemic spread is then modelled by means of derivation of strings using the 2D stochastic context free grammar. The results are then compared with the Markov Chain model of estimating the epidemic states during each time step. The following figures depicts the Markov chain transition matrix for the SIR Model.

	S	I	R
S	P_{SS}	P_{SI}	P_{SR}
I	P_{IS}	P_{II}	P_{IR}
R	P_{RS}	P_{RI}	P_{RR}

Table[4.3] Markov Chain Transition Matrix

where P is considered to be the probability of changing the state at time t to a state at time t+1.

5.0 Conclusion

Cellular automata based computational modeling is done on SIR epidemic spread with all variations of cellular automata such as 1D, 2D , 3D, 1D pushdown, and 2D pushdown CA. A 2D stochastic context free grammar is also derived for representing the population in terms of language and matched with the real time epidemic spread data and the nature of SIR epidemic behavior.

6.0 List of Publications

Senthil Athithan, Vidya Prasad Shukla, and Sangappa Ramachandra Biradar, "Epidemic Spread Modeling with Time Variant Infectives using Pushdown Cellular Automata," Journal of Computational Environmental Sciences, vol. 2014, Accepted.

Senthil Athithan, Vidya Prasad Shukla, and Sangappa Ramachandra Biradar, "Dynamic Cellular Automata Based Epidemic Spread Model for Population in Patches with Movement," Journal of Computational Environmental Sciences, vol. 2014, Article ID 518053, 8 pages, 2014. doi:10.1155/2014/518053.

A. Senthil, V.P. Shukla, S.R. Biradar, "Finite Automata for SIR Epidemic Model", International Journal of Engineering Research and Technology, Vol.2 - Issue 9 (September - 2013).

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Yang CW. (2007). Leptospirosis in Taiwan-an underestimated infectious disease. *Chang Gung Med. J.*, 109-15.

Proposed Chapters in the Thesis.

Chapter 1. Basic Cell States using Finite Automata.

Chapter 2. One Dimensional Cellular Automata Model.

Chapter 3. Two Dimensional Cellular Automata Model.

Chapter 4. Cellular Automata Model for Patch Population.

Chapter 5. Pushdown Cellular automata Model for Infectives with Time delay.

Chapter 6. Cellular Automata Model for Vector Borne Infection.

Chapter 7. Three Dimensional Cellular Automata.

Chapter 8. Epidemic Spread Grammar.

Chapter 9. Scope of Further Research.